

FIG. 1

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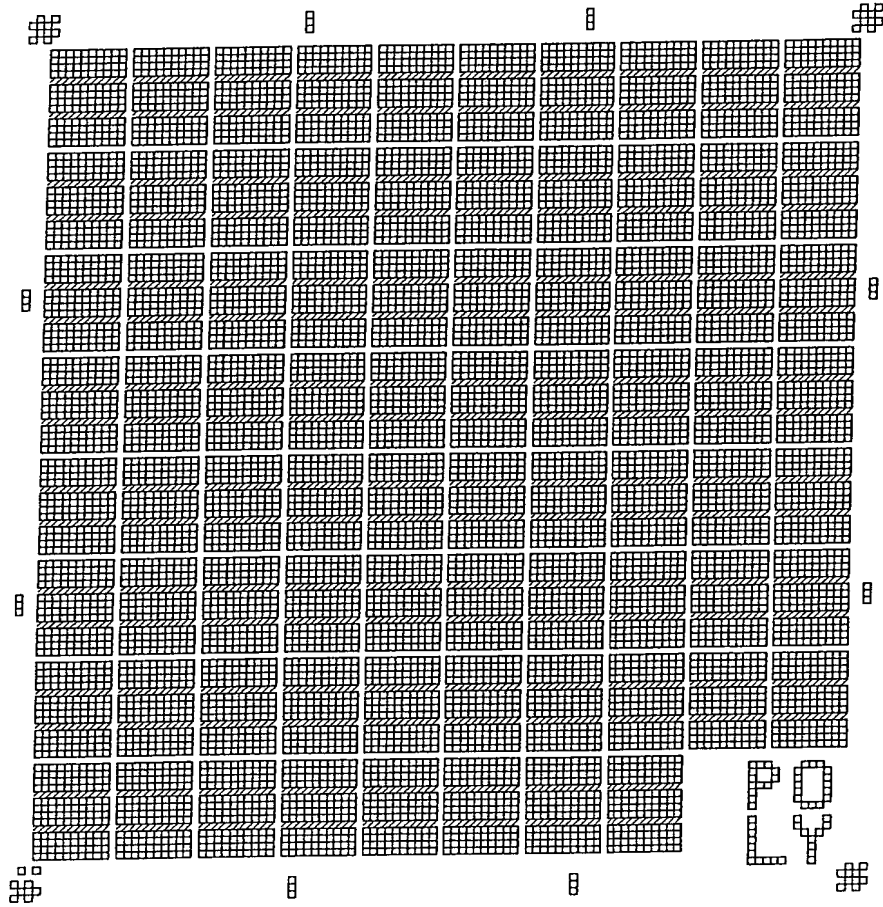
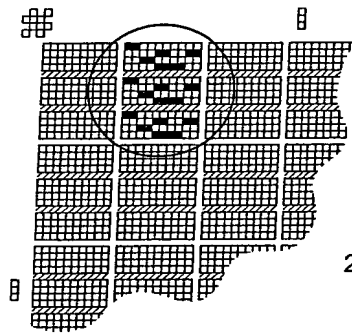


FIG. 2A

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SEQUENCE AT POLYMORPHISM WI-567

5' TGCTGCCTTGGTTC [A/G] AGCCCTCATCTCTTT 3'

THREE BLOCKS OF COMPLEMENTARY
20-MER OLIGOS WITH SUBSTITUTIONS (N)
7, 10 AND 13 BP FROM THE 3' END

	P-2	P-1	P	P+1	P+2
A	G	A	G	A	G
T					
G					
C					
A					

T					
G					
C					
A					

T					
G					
C					
A					

BASES IN THE SHADED COLUMNS

3' BLOCK 20/7 5'
AACCAAN [C] TCGGGAGTAGAG

3' BLOCK 20/10 5'
CGGAACCAAN [C] TCGGGAGTA

3' BLOCK 20/13 5'
CGACGGAACCAAN [C] TCGGGA

FIG. 2B

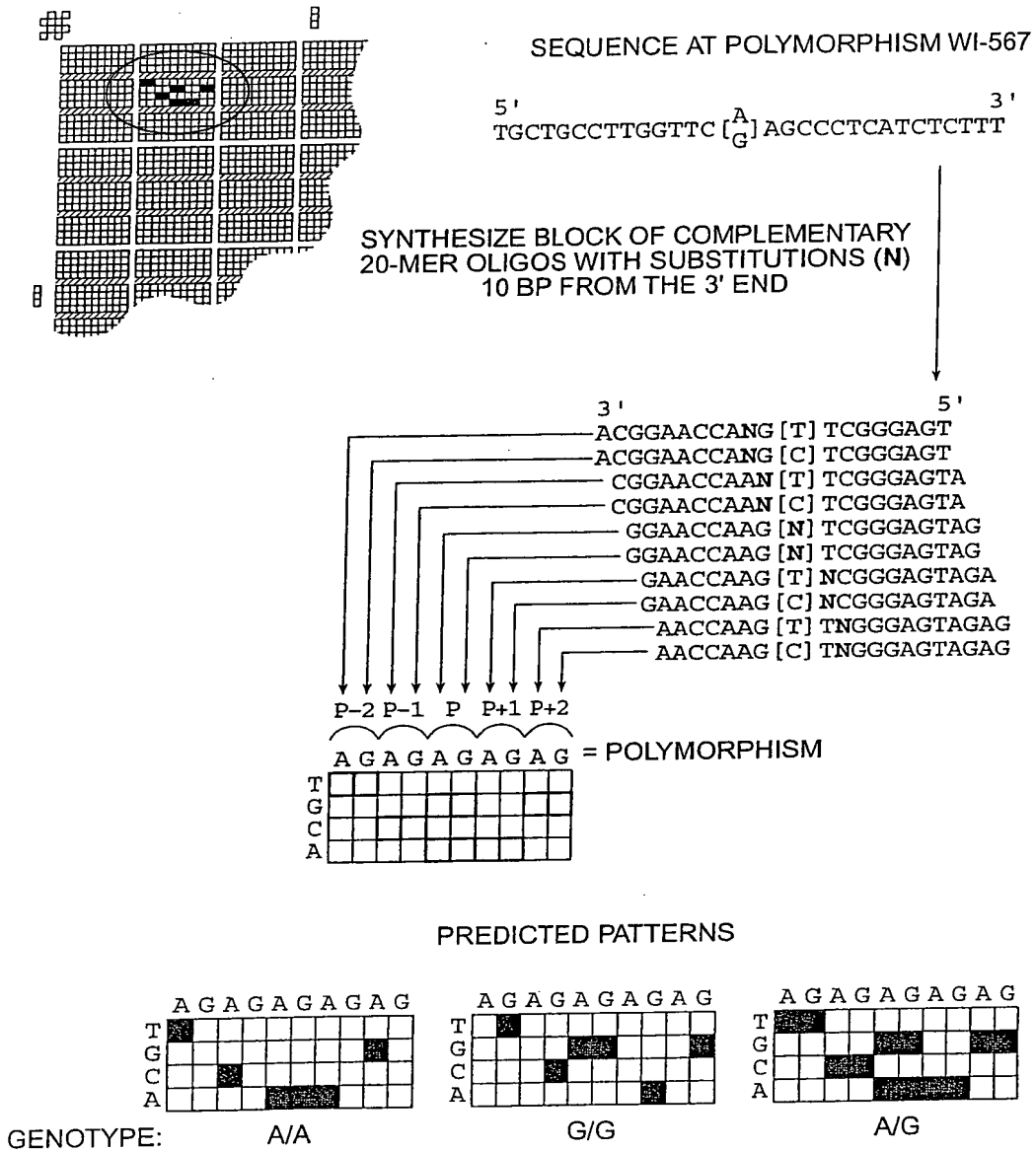


FIG. 3

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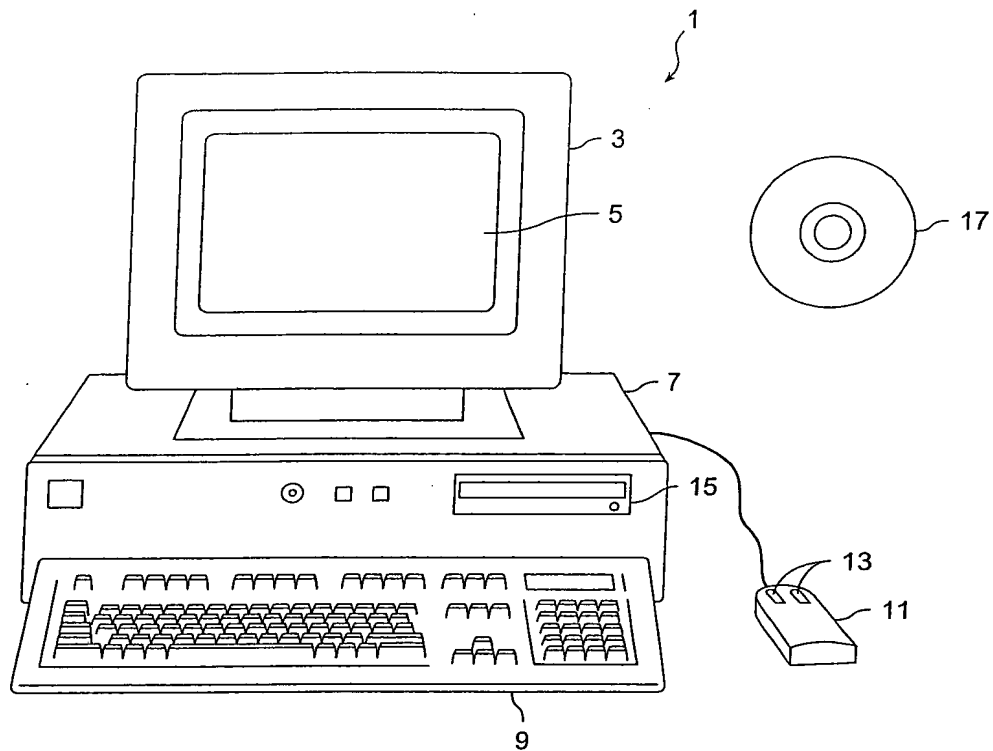


FIG. 5

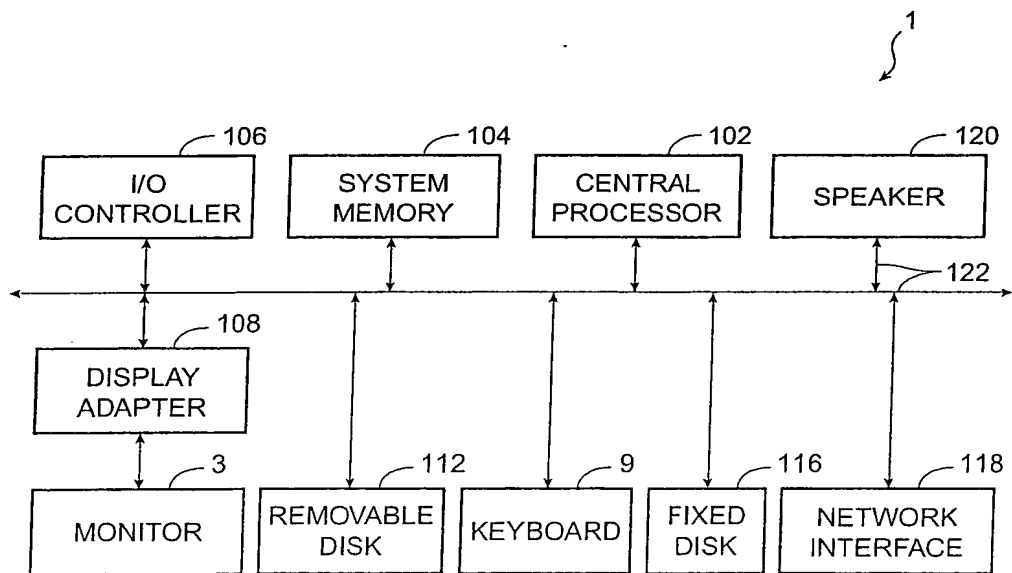


FIG. 6

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	P-2		P-1	P0	P+1	P+2	
	X	Y	X	Y	X	Y	X
A							
C							
G							
T							

FIG. 7

	T		C		A		G	
	A	G	A	G	A	G	A	G
A	nd	nd	nd	nd	nd	nd	nd	nd
C	nd	nd	nd	nd	nd	nd	nd	nd
G	nd	nd	nd	nd	nd	nd	nd	nd
T	nd	nd	nd	nd	nd	nd	nd	nd

FIG. 8

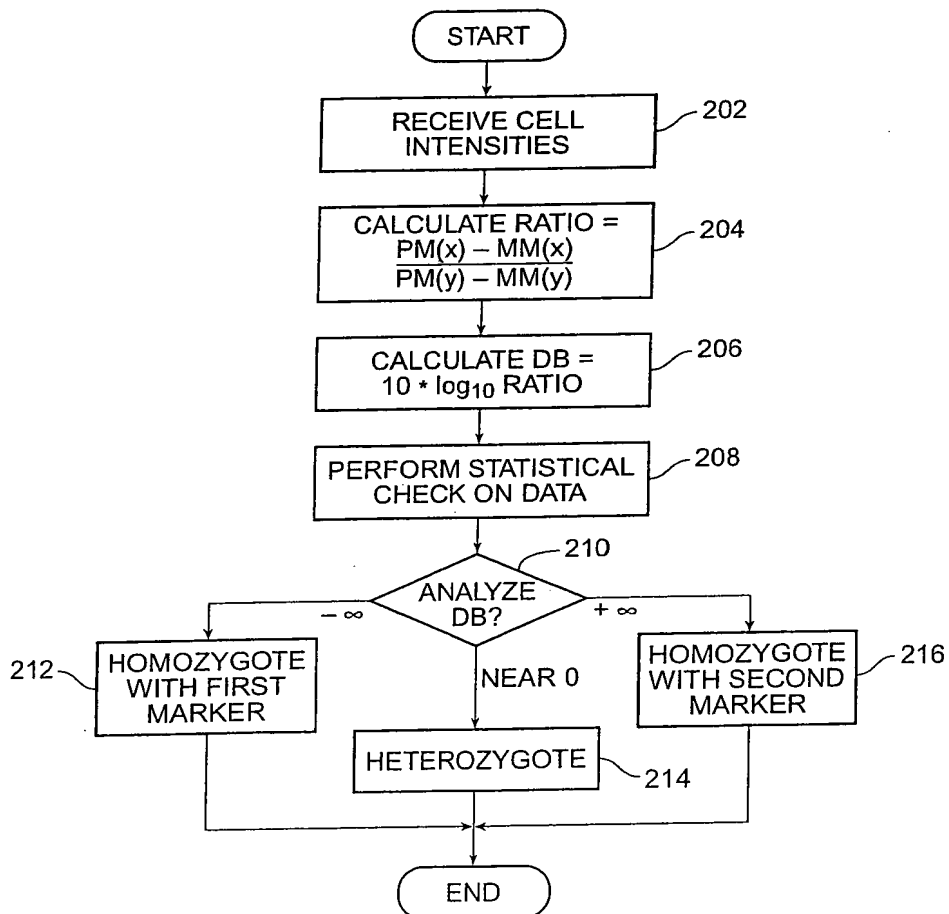


FIG. 9

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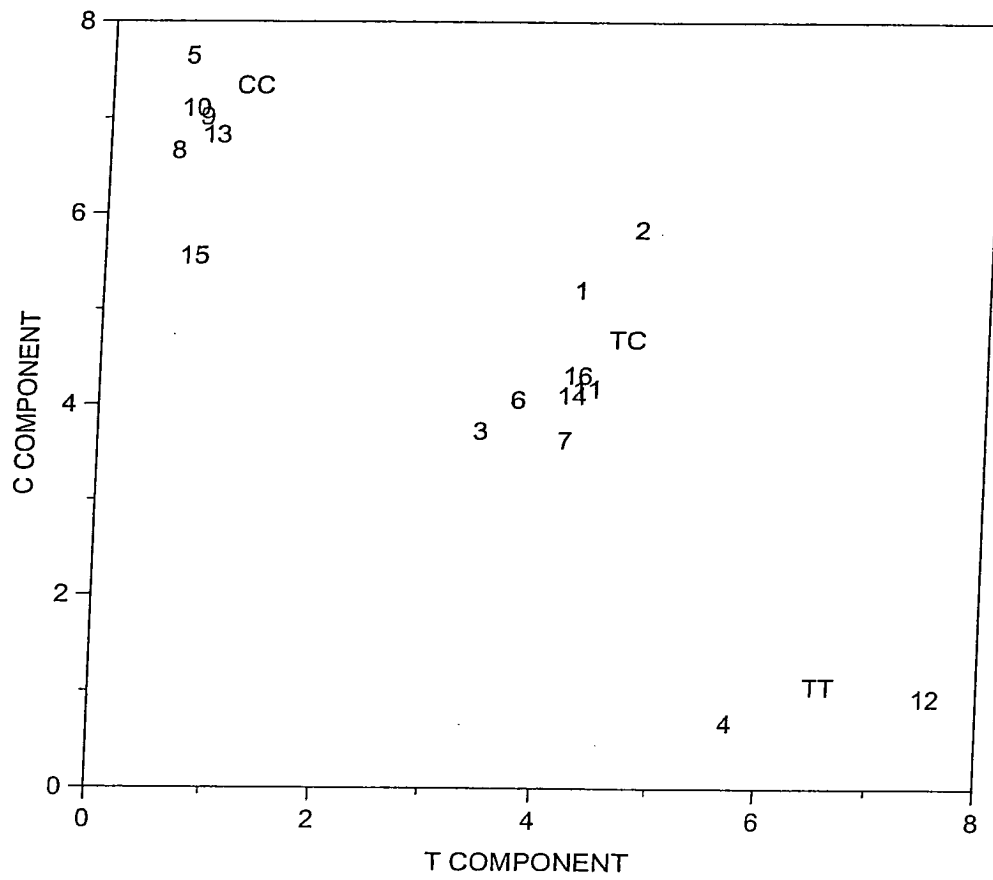


FIG. 10

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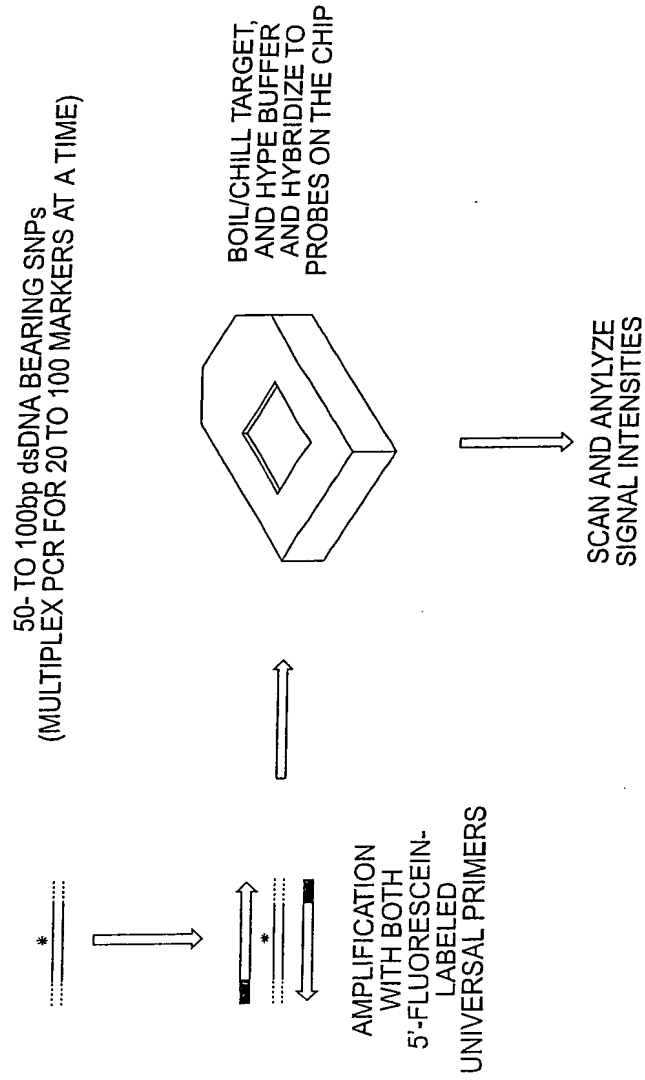


FIG. 11

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$$\begin{aligned}
 \text{DB} &= \text{"DECIBELS"} & &= 10 \times \text{LOG (DETECTION RATIO)} \\
 \text{DETECTION RATIO} &= \frac{\text{A PERFECT MATCH} - \text{A MISMATCHES}}{\text{B PERFECT MATCH} - \text{B MISMATCHES}} \\
 \text{C} = \text{SIGNIFICANCE CHECK} &= \frac{\text{MAX (A OR B PERFECT MATCH)}}{\sigma (\text{A OR B MISMATCHES})} > 2 \\
 \text{P} = \text{PATTERN MATCHING} &= \frac{\text{MEAN [MAX (A OR B PERFECT MATCHES)]}}{\text{MEAN [MAX (A OR B MISMATCHES)]}} > 1.2
 \end{aligned}$$

PREDICTED PATTERNS

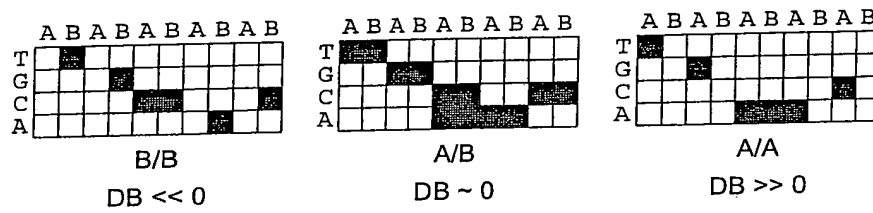


FIG. 12

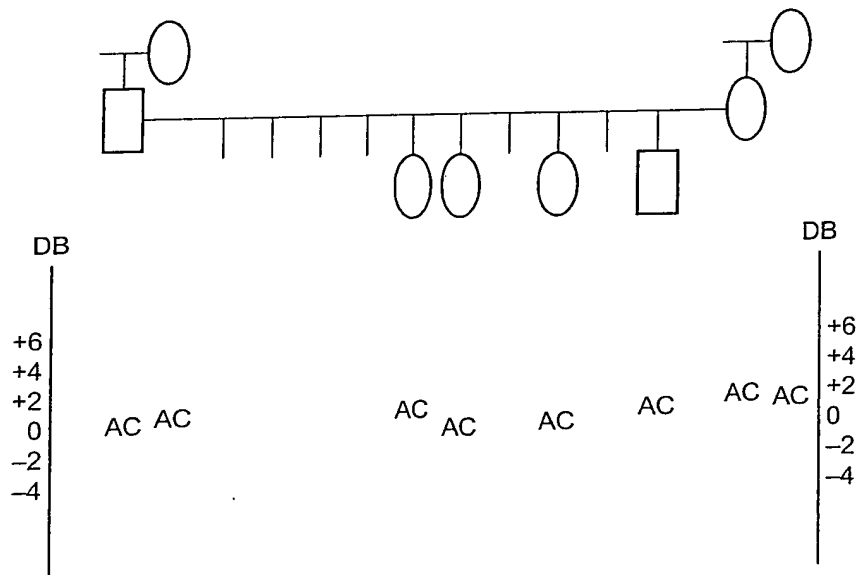


FIG. 13

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